(b) contacting said target-oligonucleotide hybrid complexes with a nuclease; thereby removing target-oligonucleotide complexes which are not perfectly complementary; and

(c) determining which of said oligonucleotides have specifically interacted with subsequences in said target nucleic acid to determine the sequence of said target nucleic acid.

17. (Amended) A method for sequencing a target nucleic acid, ~~said method~~ comprising:

(a) combining:

(i) a substrate comprising an array of chemically synthesized and positionally distinguishable oligonucleotides each of which binds to a defined subsequence of preselected length; and

(ii) a target nucleic acid which is longer than each of said probes; thereby forming target-oligonucleotide hybrid complexes of complementary subsequences of known sequence with a 3' target overhang;

(b) contacting said target-oligonucleotide hybrid complexes with a ligase and a labelled, ligatable oligonucleotide probe;

(c) removing said target nucleic acid and labelled, [unligatable] unligated oligonucleotide probes; and

(d) determining which of said oligonucleotides contain said labelled, ligatable oligonucleotide probe as an indication of a subsequence which is perfectly complementary to a subsequence of said target nucleic acid, thereby determining the sequence of said target nucleic acid.

REMARKS

Claims 1-17 are pending in the above-referenced patent application; claims 1-17 are currently under examination. The specification and claims 1 and 17 have been amended.

More particularly, the specification and claim 17 have been amended to correct minor typographical and spelling errors present in the application as originally filed. Such amendments correct merely formal matters and, thus, they embrace no new matter. Claims 1 and 17 have been amended, at the Examiner's request, to set forth the accomplishment of